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OM nucleic - nucleic search, using sw model
Run on: June 3, 2003, 13:38:24 ; Search time 3711.97 Seconds
(without alignments)
11219.411 Million cell updates/sec

Title: US-09-576-424-3
Perfect score: 1431
Sequence: 1 atgaacaacctgtgtgtttt.....ccctgtctccgggtaaatga 1431

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank

- 1: gb.ba.*
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- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.vi.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.or.*
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- 22: em.ov.*
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- 34: em.htg.pln.*
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- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1431	100.0	1431	6	AR108863 Sequence
2	1315.8	91.9	1431	6	AR108867 Sequence
3	1237.2	86.5	1431	6	E10697 cDNA encodi
4	1234.8	86.3	1567	6	AR135359 Sequence
5	1227.6	85.8	1596	6	AK098516 Homo sapi
6	1221.6	85.4	1418	6	AK9389 Sequence 7
7	1215.2	84.9	1594	9	AK057754 Homo sapi
8	1210.4	84.6	1418	6	AR176296 Sequence
9	1209.6	84.5	1589	9	AK057775 Homo sapi
10	1171.4	81.9	1404	6	AR135375 Sequence
11	1170	81.8	1566	9	AK097365 Homo sapi
12	1168.2	81.6	1404	6	AR135377 Sequence
13	1166.6	81.5	1404	6	AR135376 Sequence
14	1125.8	78.7	1633	9	AK097859 Homo sapi
15	1124.2	78.6	1507	6	BD000501 Process f
16	1123.6	78.5	1428	6	AR031184 Sequence
17	1123.6	78.5	1428	6	AR042589 Sequence
18	1123.6	78.5	1428	6	AR059282 Sequence
19	1123.6	78.5	1428	6	AR076260 Sequence
20	1122.8	78.5	1430	6	AX19496 Sequence
21	1117.4	78.1	1679	9	BC018747 Homo sapi
22	1117.2	78.1	1437	6	AR108865 Sequence
23	1116.2	78.0	1624	9	HSIGG1KH
24	1115.4	77.9	1630	9	BC024289 Homo sapi
25	1113.2	77.8	1673	9	HSIGG1LH
26	1113.2	77.8	3143	9	BC019046 Homo sapi
27	1112.4	77.7	1428	6	AR031186 Sequence
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30	1112.4	77.7	1428	6	AR076262 Sequence
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33	1104.6	77.2	1465	10	S79307 Ig gamma =1
34	1103.6	77.1	1617	6	A29585 H.sapiens c
35	1102	77.0	1599	6	AX330501 Sequence
36	1102	77.0	1599	6	AX333307 Sequence
37	1102	77.0	1599	6	AX334122 Sequence
38	1102	77.0	1599	9	HUMIGHEPAH
39	1096.4	76.6	1633	9	AK097367 Homo sapi
40	1096	76.6	7521	6	AK080951 Sequence
41	1095.6	76.6	1549	6	A21385 Plasmid DNA
42	1092.6	76.4	6557	6	I26929 Sequence 3
43	1092.4	76.3	1666	9	BC006402 Homo sapi
44	1091.8	76.3	1341	6	A07562 DNA sequenc
45	1091.4	76.3	1639	9	AK097950 Homo sapi

ALIGNMENTS

RESULT 1
AR108863
LOCUS AR108863 1431 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6113898.
ACCESSION AR108863
VERSION AR108863.1 GI:12825139
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1431)
AUTHORS Anderson,D.R., Brame,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE Human B7.1-specific primatized antibodies and transfectomas
expressing said antibodies
JOURNAL Patent: US 6113898-A 3 05-SEP-2000;

FEATURES Location/Qualifiers
source 1..1431
BASE COUNT 322 a 469 c 380 g 260 t
ORIGIN

Query Match 100.0%; Score 1431; DB 6; Length 1431;
Best Local Similarity 100.0%; Pred. No. 4.6e-280;
Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACACCTGCTGGTCTCTCCCTGCTGGTGGAGCTCCAGATGGTCTGCTCCAG 60
DB 1 ATGAACACCTGCTGGTCTCTCCCTGCTGGTGGAGCTCCAGATGGTCTGCTCCAG 60

QY 61 GTGAAGCTGAGAGTGGGGGCAAGGACTTCTGACGCTTCGGAGACCTGCTCCGAC 120
DB 61 GTGAAGCTGAGAGTGGGGGCAAGGACTTCTGACGCTTCGGAGACCTGCTCCGAC 120

QY 121 TGGTGTCTGCTGGTGGCTCCATGACGGTTACTACTGACCTGGATCCGACACC 180
DB 121 TGGTGTCTGCTGGTGGCTCCATGACGGTTACTACTGACCTGGATCCGACACC 180

QY 181 CAGGGAGGGGACTGAGTGGATGGCCATATTTATGTTGGTGGAGCACTAC 240
DB 181 CAGGGAGGGGACTGAGTGGATGGCCATATTTATGTTGGTGGAGCACTAC 240

QY 241 AATCCCTCCCTCAAGAGTGGAGTCAACATTTCAAAGACACGCTCAAGAACCAAGTTCTTC 300
DB 241 AATCCCTCCCTCAAGAGTGGAGTCAACATTTCAAAGACACGCTCAAGAACCAAGTTCTTC 300

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QY 361 CGCCCTGATGACACACCATTTGTTATGGGCTGGTGCATGCTGGGGCCGGAGAC 420
DB 361 CGCCCTGATGACACACCATTTGTTATGGGCTGGTGCATGCTGGGGCCGGAGAC 420

QY 421 CTGGTCACCGTCTCCTCAGTACGACCAAGGGCCCTGCTTCCCTCCGACCCCTCC 480
DB 421 CTGGTCACCGTCTCCTCAGTACGACCAAGGGCCCTGCTTCCCTCCGACCCCTCC 480

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DB 481 TCAAGAGACCTCTGGGGGCAAGCGGCTGGGCTGCTGGTCAAGGACTACTTCC 540

QY 541 GAACGGTACCGTGGTGGAGTCAAGGCGCTGACCGGGGTCACACCTTCCG 600
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DB 601 GCTGTCTACAGTCTCAGGACTTACTCCCTCAGCAGGCTGGTGAACCTCCAGC 660

QY 661 AGCTGGGACCCAGACCTTACATCTGCAACGTAATCAAGCCCAAGCAACCAAGGTG 720
DB 661 AGCTGGGACCCAGACCTTACATCTGCAACGTAATCAAGCCCAAGCAACCAAGGTG 720

QY 721 GACAGAAAGCAGAGCCCAATCTTGTGACAACTCAACATGCCCGTGGCCAGCA 780
DB 721 GACAGAAAGCAGAGCCCAATCTTGTGACAACTCAACATGCCCGTGGCCAGCA 780

QY 781 CTTGAACCTCTGGGGGACCGTCACTTCTCTTCCCTCCCAAAACCCAGGACACCTTC 840
DB 781 CTTGAACCTCTGGGGGACCGTCACTTCTCTTCCCTCCCAAAACCCAGGACACCTTC 840

QY 841 ATGATCTCCCGACCCCTGAGTCAATGCGTGGTGGAGCTGAGCCACCAAGACCT 900
DB 841 ATGATCTCCCGACCCCTGAGTCAATGCGTGGTGGAGCTGAGCCACCAAGACCT 900

QY 901 GAGGTCAAGTCTCACTGGTACCTGGACGCGGTGGAGTGCATATGCCAAGCAAGCCG 960
DB 901 GAGGTCAAGTCTCACTGGTACCTGGACGCGGTGGAGTGCATATGCCAAGCAAGCCG 960

QY 961 CGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTACGCTCTCACCGTCTGCAACCAG 1020
DB 961 CGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTACGCTCTCACCGTCTGCAACCAG 1020

QY 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGAAGTCTCCAACAAGACCTCCAGCCCC 1080
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DB 1141 CCCCCATCCCGGATGAGTGAACCAAGAACCAAGGTGACCTGCTGCTGCTCAAGGC 1200

QY 1201 TTCTATCCAGGACATCGCGTGGAGTGGAGAGCAATGGGACCCGGAGAACAACTAC 1260
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QY 1261 AAGACACGCTCCCGTGTGAGTCCGACGCTCTTCTTCTCTACGAAAGTCAACC 1320
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QY 1321 GTGGAACAGAGCAGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTCGTCATGAGCT 1380
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QY 1381 CTGCACAACTACTACGACAGAGGCTCTCCCTGCTCCGGTAAATGA 1431
DB 1381 CTGCACAACTACTACGACAGAGGCTCTCCCTGCTCCGGTAAATGA 1431

RESULT 2
ARI08867
LOCUS ARI08867 1431 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6113898.
ACCESSION ARI08867
VERSION ARI08867.1 GI:12825143
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1431)
AUTHORS Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE Human B7.1-specific primatized antibodies and transfectomas
JOURNAL expressing said antibodies
FEATURES Patent: US 6113898-A 11 05-SEP-2000;
Location/Qualifiers
source 1..1431
/organism="unknown"

BASE COUNT 319 a 462 c 385 g 265 t
ORIGIN

Query Match 91.9%; Score 1315.8; DB 6; Length 1431;
Best Local Similarity 95.0%; Pred. No. 1.1e-256;
Matches 1359; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1 ATGAACACCTGCTGGTCTCTCCCTGCTGGTGGAGCTCCAGATGGTCTGCTCCAG 60
DB 1 ATGAACACCTGCTGGTCTCTCCCTGCTGGTGGAGCTCCAGATGGTCTGCTCCAG 60

QY 61 GTGAAGCTGAGAGTGGGGGCAAGGACTTCTGACGCTTCGGAGACCTGCTCCGAC 120
DB 61 GTGAAGCTGAGAGTGGGGGCAAGGACTTCTGACGCTTCGGAGACCTGCTCCGAC 120

QY 121 TGGTGTCTGCTGGTGGCTCCATGACGGTTACTACTGACCTGGATCCGACACC 180
DB 121 TGGTGTCTGCTGGTGGCTCCATGACGGTTACTACTGACCTGGATCCGACACC 180

QY 181 CAGGGAGGGGACTGAGTGGATGGCCATATTTATGTTGGTGGAGCACTAC 240
DB 181 CAGGGAGGGGACTGAGTGGATGGCCATATTTATGTTGGTGGAGCACTAC 240

Db	181	CGAGGAAGGGGCTGGAGTGGATTGGGAGTTTCTATATAGTAGTAGTGGGAACA	CCTACTAC	240
Qy	241	AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAGACACGCTCCAAAGAAC	CAGTTCCTTC	300
Db	241	AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTC	CAAGAACCACTCTCC	300
Qy	301	CTGAACCTTGAAATCTGTGACGAGCGGGACACGGCCGCTCTATTACTGTGCGAGAGCCCT	360	
Db	301	CTGAAGCTGAATCTATGACCGCGCGGGACACGGCCGCTGTATTACTGTGTGAGAGATCGT	360	
Qy	361	CGCCCTGATTGACAAACATTTGTTATGGCGGCTGGGTCGATGTC	TGGGCGCCCGGGAGAC	420
Db	361	CTTTTTTCAGTTGTGGAATGGTTTCAACAACTGGTTCGATGTC	TGGGCGCCCGGGAGTC	420
Qy	421	CTGTCACCGGCTCTCTCAGCTAGCACCAAGGGGCCCATCGGTCTTTC	CCCTCGCACCCCTCC	480
Db	421	CTGGTCACCGGCTCTCTCAGCTAGCACCAAGGGGCCCATCGGTCTTTC	CCCTCGCACCCCTCC	480
Qy	481	TCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCCTGTGTC	TAAGGACTACTTCCCC	540
Db	481	TCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCCTGTGTC	TAAGGACTACTTCCCC	540
Qy	541	GAACCGGTGACGGTGCCTGGAACTCAGGCGCCCTGACAGCGCGCTGAC	ACTTATTC	600
Db	541	GAACCGGTGACGGTGCCTGGAACTCAGGCGCCCTGACAGCGCGCTGAC	ACTTATTC	600
Qy	601	GCTGTCCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC	CGCTCCCTCCAGC	660
Db	601	GCTGTCCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC	CGCTCCCTCCAGC	660
Qy	661	AGCTTGGGACCCAGACCTTCACTCTCAAGCGTGAATCAAGGCCAGCA	ACCAAGGTG	720
Db	661	AGCTTGGGACCCAGACCTTCACTCTCAAGCGTGAATCAAGGCCAGCA	ACCAAGGTG	720
Qy	721	GACAAGAAAGCAGAGCCCAATCTTGTCGAACAACACTCACATGCCCAC	CGTGC	780
Db	721	GACAAGAAAGCAGAGCCCAATCTTGTCGAACAACACTCACATGCCCAC	CGTGC	780
Qy	781	CCTGAACTCTCTGGGGGACCGTCAGTCTTCTTCTTCCCCCAAAAC	CCAAAGGACACCCCTC	840
Db	781	CCTGAACTCTCTGGGGGACCGTCAGTCTTCTTCTTCCCCCAAAAC	CCAAAGGACACCCCTC	840
Qy	841	ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGACGTCGAGCC	ACGAGACCCCT	900
Db	841	ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGACGTCGAGCC	ACGAGACCCCT	900
Qy	901	GAGTCAAGTTCAACTGGTACGTCGAGCGGCGTGGAGGTGCATATG	CCAGACAAAGCCG	960
Db	901	GAGTCAAGTTCAACTGGTACGTCGAGCGGCGTGGAGGTGCATATG	CCAGACAAAGCCG	960
Qy	961	CGGAGGAGCAGTACAAACAGCACGTACCGTGGTGGTGGTGGTGGTGG	TCCTCAGCGTCTGACCCAG	1020
Db	961	CGGAGGAGCAGTACAAACAGCACGTACCGTGGTGGTGGTGGTGGTGG	TCCTCAGCGTCTGACCCAG	1020
Qy	1021	GACTGGCTGAATGSCAAGGAGTACAAGTGAAGGTCTTCAAACAAAG	CCCTCCAGCC	1080
Db	1021	GACTGGCTGAATGSCAAGGAGTACAAGTGAAGGTCTTCAAACAAAG	CCCTCCAGCC	1080
Qy	1081	ATCGAGAAAACCATCTCTCAAAGCCAAAGGGGACCCCGAGAAC	CCAGGTGTACCCCTG	1140
Db	1081	ATCGAGAAAACCATCTCTCAAAGCCAAAGGGGACCCCGAGAAC	CCAGGTGTACCCCTG	1140
Qy	1141	CCCCATCCCGGGATGAGCTGACCAAGAACAGGTACAGCTGACCT	GCCTGGTCAAGGC	1200
Db	1141	CCCCATCCCGGGATGAGCTGACCAAGAACAGGTACAGCTGACCT	GCCTGGTCAAGGC	1200
Qy	1201	TTCTATCCAGCGCATCGCCGTGGAGTGGGAGCAATGGCAGCGCG	AGAGAACCACTAC	1260
Db	1201	TTCTATCCAGCGCATCGCCGTGGAGTGGGAGCAATGGCAGCGCG	AGAGAACCACTAC	1260
Qy	1261	AAGACACAGCCCTCCCGTGTGGACTCCGACGGCTCTTCTTCTTAC	GACGAACTCAAC	1320
Db	1261	AAGACACAGCCCTCCCGTGTGGACTCCGACGGCTCTTCTTCTTAC	GACGAACTCAAC	1320

Qy	1321	GTGCACAAGACGAGCTGGCGACAGAGGGGAACGCTCTTCTCATGCTCCGTCATGCAATGAGGCT	1380
Dd	1321	GTGCACAAGACGAGCTGGCGACAGAGGGGAACGCTCTTCTCATGCTCCGTCATGCAATGAGGCT	1380
Qy	1381	CTGCACAACCACTACACGACGAGAAGAGCCTCTCCCTGCTCTCCGGGTAAATGA	1431
Dd	1381	CTGCACAACCACTACACGACGAGAAGAGCCTCTCCCTGCTCTCCGGGTAAATGA	1431
RESULT 3	E10697	1431 bp RNA linear PAT 29-SEP-1997	
LOCUS	E10697	cDNA encoding heavy chain of human monoclonal antibody against human cytomegalovirus 65KD antigen.	
DEFINITION	E10697		
ACCESSION	E10697		
VERSION	E10697.1	GI:22027790	
KEYWORDS	JP 19960318178-A/20.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1431)		
TITLE	Tanaka,S., Niwa,H. and Tanaka,H.		
JOURNAL	HUMAN MONOCLONAL ANTIBODY AND PRODUCTION THEREOF, AND PRIMER FOR CLONING OF GENE THEREOF		
COMMENT	Patent: JP 19960318178-A 20 13-FEB-1996; TANAKA HIDEYUKI, NISSHINO IND INC OS Homo sapiens (human) PN JP 19960318178-A/20 PD 13-FEB-1996 PF 20-FEB-1995 JP 1995030742 PR 18-FEB-1994 JP 94F 21628 PI TANAKA SHIGEAKI, NIWA HIROKUNI, TANAKA HIDEYUKI PC C12N15/09,C07K16/08,C12N15/21,C12P21/08,C12Q1/68, PC G01N33/53, PC G01N33/531,G01N33/577,(C12N1/21,C12R1:19),(C12P21/08, PC C12R1:19); CC strandedness: Single; CC topology: Linear; CC hypothetical: No; CC anti-sense: No; FH Key Location/Qualifiers EH FT source 1..1431 /organism='Homo sapiens' FT /cell_type='B cell' FT sig_peptide 1..57 /product='signal peptide of heavy chain of FT FT human monoclonal antibody against human cytomegalovirus 65KD FT mat_peptide 58..1425 /product='heavy chain of human monoclonal FT FT antibody against human cytomegalovirus 65KD antigen' FT CDS FT 1..1428 /product='heavy chain of human monoclonal FT FT antibody against human cytomegalovirus 65KD antigen' FT 3'UTR FEATURES source 1429..>1431. Location/Qualifiers 1..1431 /organism="Homo sapiens" /db_xref="taxon:9606" BASE COUNT 314 a 475 c 379 g 263 t ORIGIN Query Match 86.5%; Score 1237.2; DB 6; Length 1431; Best Local Similarity 92.9%; Pred. No. 9.1e-241; Matches 1332; Conservative 0; Mismatches 93; Indels 9; Gaps 3; Qv 1 ATGAACACACTGTTGGTTCTTCTCTCTCTGGTGACAGCTCCCAGATGGGTCTGTGCCAG 60		

361	Db	AAATGGAAGTATCATTGGGGACTGGTTGCAACCCCTGGGGCCAAAGTACCACTGTCAACCGTC	420
433	Qy	TCCTCAGCTAGCACAAAGGGCCCATCGGTCTTCCCTCTGGCACCTCTCTCAAAGAGCACCC	492
421	Db	TCCTCAGCTCCACCAAGAGGCCCATCGGTCTTCCCTCTGGCACCTCTCTCAAAGAGCACCC	480
493	Qy	TCTGGGGGCAACAGGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTGACG	552
481	Db	TCTGGGGGCAACAGGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTGACG	540
553	Qy	GTGTCGTGGAACTCAGCGCCCTGTACACAGCGGGGTGCACACCTTCCCGGCTGTCTTACAG	612
541	Db	GTGTCGTGGAACTCAGCGCCCTGTACACAGCGGGGTGCACACCTTCCCGGCTGTCTTACAG	600
613	Qy	TCCTCAGGACTTACTCCCTCAGCAGCGTGTGTACACCTGCGCTCCAGCAGCTTGGGCACC	672
601	Db	TCCTCAGGACTTACTCCCTCAGCAGCGTGTGTACACCTGCGCTCCAGCAGCTTGGGCACC	660
673	Qy	CAGACTTACATCTGCAACGTGAATATCAAGCCGACGAAACCAAGGTGGGACAAAGACA	732
661	Db	CAGACTTACATCTGCAACGTGAATATCAAGCCGACGAAACCAAGGTGGGACAAAGACA	720
733	Qy	GAGCCCAAACTTGTGACAAACTCACACATGCCCAACCGTGCCAGCAGCACTGAACCTCTG	792
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853	Qy	ACCCCTGAGGTACATCGTGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTC	912
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913	Qy	AACCTGTACGTGGACGGGTGGAGTGCATAATGCCAAGCAAGCCGCGGGAGGAGCAG	972
901	Db	AACCTGTACGTGGACGGGTGGAGTGCATAATGCCAAGCAAGCCGCGGGAGGAGCAG	960
973	Qy	TACAAACAGCAGTACCCGTGTGGTCAGCGTCTCTACCCGTCTGCAACCAAGCACTGGCTGAAT	1032
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1021	Db	GGCAAGGAGTACAAGTGCAGAGTCTCAAACAAAGCCCTCCACGCCCCCATCGAGAAAACC	1080
1093	Qy	ATCTCCAAAGCCAAAGGGACCCCGAGAACCAACAGGTGTACACCTGTGCCCCCATCCCGG	1152
1081	Db	ATCTCCAAAGCCAAAGGGACCCCGAGAACCAACAGGTGTACACCTGTGCCCCCATCCCGG	1140
1153	Qy	GATGAGCTGACCAAGAACCAAGTTCAGCTGTGACCTGTGCTGCTCAAGAGCTTCTATCCGAGC	1212
1141	Db	GATGAGCTGACCAAGAACCAAGTTCAGCTGTGACCTGTGCTGCTCAAGAGCTTCTATCCGAGC	1200
1213	Qy	GACATCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACCACTACAAGACCAACGCT	1272
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1273	Qy	CCCGTGTGACTCCGACGGCTCTCTTCTCTACAGCAAGTTCACCGTGGGACAGAGC	1332
1261	Db	CCCGTGTGACTCCGACGGCTCTCTTCTCTACAGCAAGTTCACCGTGGGACAGAGC	1320
1333	Qy	AGTGGCAGCAGGGGAACGCTTCTCATGTCTCGTGTATGATGATGAGGCTCTGCAACAACAC	1392
1321	Db	AGTGGCAGCAGGGGAACGCTTCTCATGTCTCGTGTATGATGATGAGGCTCTGCAACAACAC	1380
1393	Qy	TACACGAGAAGAGCCCTCTCCCTGTCTCCCGGTAAATG	1430
1381	Db	TACACGAGAAGAGCCCTCTCCCTGTCTCCCGGTAAATG	1418

RESULT 7
AK057754

RESULT 7
AK057754

LOCUS AK057754 1594 bp mRNA linear PRI 27-MAR-2002
DEFINITION Homo sapiens cDNA FLJ25025 fis, clone CBL01928, highly similar to Ig gamma immunoglobulin heavy chain.
ACCESSION AK057754
VERSION AK057754.1 GI:16553681
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL clone:CBL01928.H
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Nishi,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano.S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
PUBLISHED 2 (bases 1 to 1594)
AUTHORS Sugano,S. and Suzuki,Y.
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COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.

FEATURES
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CDS
BASE COUNT 338 a 532 c 437 g 287 t

ORIGIN
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Best Local Similarity 92.0%; Pred. No. 2.6e-236;
Matches 1319; Conservative 0; Mismatches 103; Indels 12; Gaps 3;

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333	Db	TTCT	CTGACACTGACCTCTGTGACCGCCGCGGATACGGCTGTCTATTACTGTGTGGAGA---	389
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478	Qy	TCCT	CCAAGACACCTCTGGGGGACACAGCGCCCTGGGCTGCTGTGTCAAAGACTACTTC	537
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538	Qy	CCCG	AAACCGGTGACGGTGTCTGTGAACTCTCAGCGCCCTGACCAAGCGCGGTGCACACCTTC	597
567	Db	CCCG	AAACCGGTGACGGTGTCTGTGAACTCTCAGCGCCCTGACCAAGCGCGGTGCACACCTTC	626
598	Qy	CCG	CTGTCTACAGTCTCTCAGGACTCTACTCTCTCAGCAGCGGTGTGACCGTGCCTCTCC	657
627	Db	CCG	CTGTCTACAGTCTCTCAGGACTCTACTCTCTCAGCAGCGGTGTGACCGTGCCTCTCC	686
658	Qy	AGCA	GCTTTGGCACCCAGACTCATCTGTGCAACTGTGAATTCAGAGCCCGGCAACACCAAG	717
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1107	Db	CCCA	TCAGAAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACAC	1166
1138	Qy	CTG	CCCCCATCTCCGGGATGAGCTACCAAGAAACCAAGTTCAGCCTTGAACCTGTCTGGTCAAA	1197
1167	Db	CTG	CCCCCATCTCCGGGATGAGCTACCAAGAAACCAAGTTCAGCCTTGAACCTGTCTGGTCAAA	1226
1198	Qy	GGCT	TTCTATCCACGCAATCGCGTGTGGAGTGGGAGCAATGGGACCGGAGCAAC	1257
1227	Db	GGCT	TTCTATCCACGCAATCGCGTGTGGAGTGGGAGCAATGGGACCGGAGCAAC	1286

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QY	1318	ACCGTGACACAGACGAGTCCGACGAGGGAACGTCTTCTCATGCTCCGTGATGCATGAG	1377			
Db	1347	ACCGTGACACAGACGAGTCCGACGAGGGAACGTCTTCTCATGCTCCGTGATGCATGAG	1406			
QY	1378	GCTCTGCACAACCACTACACGACGAGAGAGCTCTCCCTGTCTCCGGTAAATGA	1431			
Db	1407	GCTCTGCACAACCACTACACGACGAGAGAGCTCTCCCTGTCTCCGGTAAATGA	1460			
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AR176296						
LOCUS	AR176296	1418 bp	DNA linear PAT 17-DEC-2001			
DEFINITION	Sequence 7 from patent US 6312690.					
ACCESSION	AR176296					
VERSION	AR176296.1 GI:17918651					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1418)					
AUTHORS	Edelman, B., Margaratte, C., Kaczorek, M. and Chaabihi, H.					
TITLE	Monoclonal recombinant anti-rhesus D (D7C2) antibody					
JOURNAL	Patent: US 6312690-A 7 06-NOV-2001;					
FEATURES	Location/Qualifiers					
source	1..1418					
BASE COUNT	332 a	454 c	253 g			
ORIGIN	/organism="unknown"					
Query Match						
Best Local Similarity 84.6%; Score 1210.4; DB 6; Length 1418;						
Matches 1310; Conservative 0; Mismatches 96; Indels 12; Gaps 3;						
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QY	73	CAGTGGGGCGAAGGACTTTCGACGCTTCGGAGACCCCTGTCCGACACCTCGCTGTCTCT	132			
Db	73	CAGTGGGGCGAGACTGTGAAGCCTTCGGAGACCTGTCCCTCACTGCACCTGTCTAT	132			
QY	133	GGTGGCTCCATCAGCGGTACTACTACTGGACCTGGATCCGCCAGACCCCGAGGGAGGGA	192			
Db	133	GGTGGGTCTTCACTGTGT---TACTACTGGAGCTGGATCCGCCAGACCCCGAGGGAGGGG	189			
QY	193	CTGAGTGGGATTTGGCCATATTTATGGTATGGTGGACACACCAACTACAACTCCCTCCCTC	252			
Db	190	CTGAGTGGGATTTGGGAAATCAA---TCATAGTGGAAAGCACCAACTACAACTCCCTCCCTC	246			
QY	253	AAGAGTCGAGTCACCATTTCAAAGACAGCTCCCAAGAACGAGTTCCTTCTTGAACCTTGAAT	312			
Db	247	AAGAGTCGAGTCACCATATCAGTAGACAGCTCCAGAACGAGTTCCTTCTTGAACCTGAAC	306			
QY	313	TCTGTGACCGACGCGGACAGCGCCGTCTATTTACTGTGCGAGAGGCGCTCGCCCTGATTGC	372			
Db	307	TCTGTGACCGCCGCGGACAGCGCTGTGTATTACTGTGCGAGGG- - - - -CCCCAGAGTAT	360			
QY	373	ACAACCATTTGTTATGGCGCTGGGTGCATGTCTGGGGCCCGGAGACCTGTGTACCGTTC	432			
Db	361	AAATGGAAGTATCATGCGGACTGGTTCGACCCCTGGGGCCCAAGGTACCACTGTCAACCGTC	420			
QY	433	TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCGCACCTCTCTCCAAAGACACC	492			
Db	421	TCCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCGCACCTCTCTCCAAAGACACC	480			
QY	493	TCTGGGGGCAAGCGGCTTGGGCTGCCTGGTCAAGGACTACTTCCCGAAACGGGTGACG	552			
Db	481	TCTGGGGGCAAGCGGCTTGGGCTGCCTGGTCAAGGACTACTTCCCGAAACGGGTGACG	540			

Qy	553	GTGTCGTGGAAC	TGAGCGGCCTGAC	CAGCGCGGTGC	ACCTTCCCGGTGCTTACAG	612
Db	541	GTGTCGTGGAAC	TGAGCGGCCTGAC	CAGCGCGGTGC	ACCTTCCCGGTGCTTACAG	600
Qy	613	TCCTCAGGACT	CTACTCCCTCAG	CAGCGTGTGAC	CGTGCCTCCACGACTTGGGCACC	672
Db	601	TCCTCAGGACT	CTACTCCCTCAG	CAGCGTGTGAC	CGTGCCTCCACGACTTGGGCACC	660
Qy	673	CAGACCTACAT	CTGCAACGTGAAT	CAACAAGCCCAG	CAACCAAGGTGGAACAAGAAGCA	732
Db	661	CAGACCTACAT	CTGCAACGTGAAT	CAACAAGCCCAG	CAACCAAGGTGGAACAAGAAGCA	720
Qy	733	GAGCCCAAAAT	CTTGTGACAAAA	CTCACATGCC	CCAGTGCACGACCTGAACCTCTG	792
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Qy	793	GGGGGACCGT	CAGCTTCTCTT	CCCCCCCAAA	CCCCCAAGGACACCTCATGATCTCCCGG	852
Db	781	GGGGGACCGT	CAGCTTCTCTT	CCCCCCCAAA	CCCCCAAGGACACCTCATGATCTCCCGG	840
Qy	853	ACCCCTGAGGT	CAATCGTGTGG	AGCTGAGCC	ACGAAGACCCCTGAGGTCAAGTTC	912
Db	841	ACCCCTGAGGT	CAATCGTGTGG	AGCTGAGCC	ACGAAGACCCCTGAGGTCAAGTTC	900
Qy	913	AACGTGTACGT	GAGCGGTGG	AGGTGCAATA	TGCCAAGACAAAGCCGCGGAGGAGCAG	972
Db	901	AACGTGTACGT	GAGCGGTGG	AGGTGCAATA	TGCCAAGACAAAGCCGCGGAGGAGCAG	960
Qy	973	TACAAACAGC	GTACCGTGTGT	GTCAGGTCTCT	CAACCGTCTGCAACAGGACTTGGCTGAAT	1032
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Qy	1033	GGCAAGGAGT	ACAAGTCAAG	GTCTCCAA	CAAAAGCCCTCCAGCCCCCATCGAGAAAAC	1092
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Qy	1333	AGGTGGCAGC	AGGGGAACGT	CTTCTCAT	GTGCTCGGTGATGATAGGCTCTGCAACACAC	1392
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RESULT 9	AK057775	1589 bp	mRNA	linear	PRI 26-MAR-2002
LOCUS	AK057775				
DEFINITION	Homo sapiens CDNA FLJ25046 fis, clone CBL03624, highly similar to Ig gamma immunoglobulin heavy chain.				
ACCESSION	AK057775				
VERSION	AK057775.1 GI:165533709				
KEYWORDS	oligo capping; fis (full insert sequence).				
SOURCE	Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL clone:CBL03624.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

814	ATGATCTCCCGGACCCCTGAGGTCAGTGGCTGGTGGAGCTGACCGAGGAAGACCCC	873
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874	GAGGTCGAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATATGCGAACAAGCCG	933
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934	CGGAGGAGGACGATTCACACAGCACGTACCGTGTGGTTCAGCGTCTTCCACGCTCTGCACAG	993
1021	GACTGGCTGAATGCGCAAGGAGTACAAGTGAAGGTCTCCAAACGAAGCCCTCCGACGCCCC	1080
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1294	GTGGACAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGTGATGCATGAGGCT	1353
1381	CTGCACAACCACTACACGCAAGAGAGCTCTTCTCTCTCCGTGCTCCGGGTAATATGA	1431
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LOCUS	AK097365	1566 bp	mRNA linear
DEFINITION	Homo sapiens cDNA FLJ40046 fig.	clone SYN0V2001300,	highly similar to Ig gamma -immunoglobulin heavy chain.

ACCESSION AK097365
VERSION AK097365.1 GI:21757092
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens synovial membrane tissue from rheumatoid arthritis
cDNA to mRNA, clone lib:SYNOV2 clone:SYNOV2001300.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Clone_ID: SINOVS0001306.

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REFERENCE
AUTHORS
TITLE
Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kodaira, H., Furiya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsura, N., Sato, K., Tanikawa, M., Yamaraki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamanoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
Kikura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project

TITLE
NEDO human cDNA sequencing project
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1566)
AUTHORS
Isogai, T. and Yamamoto, J.
TITLE
Direct Submission
JOURNAL
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
COMMENT
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' - and 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES source

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ORIGIN

Query Match 81.8%; Score 1170; DB 9; Length 1566;
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Qy	1201	TTCTATCCCGACGACATCGCCGTGCGAGTGGGAGAGCAATGGGCAGCCGAGAGAACCAACTAC	1260
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AR135376.1 GI:14476048			
KEYWORDS			
Unknown.			
SOURCE			
Unknown.			
ORGANISM			
Unclassified.			
REFERENCE			
1 (bases 1 to 1404)			
AUTHORS			
Hanna,N., Newman,R.,Anthony. and Reff,M.,Elliot.			
TITLE			
Recombinant anti-CD4 antibodies for human therapy			
JOURNAL			
Patent: US 6136310-A 9 24-OCT-2000;			
FEATURES			
Location/Qualifiers			
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/organism="unknown"			
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Query Match			
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Best Local Similarity			
89.8%; Pred. No. 1.9e-226;			
Matches 1285; Conservative 0; Mismatches 119; Indels 27; Gaps 2;			
Qy	1	ATGAAACACCTGTGGTCTTCTCTCTCTGTGTGACGCTCCAGATGGGTCTGTGTCCAG	60
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Db	1234	AAGACACGCTCCCGTGTGAGTCCGACGGCTCTCTTCTCTCTATCAGCAGGCTAACC	1293

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:15:24 ; Search time 1951.49 Seconds

(without alignments)
11875.950 Million cell updates/sec

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Scoring table:

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Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2	864	60.4	947	14	BQ709771
3	850.4	59.4	958	14	BQ706140
4	842.4	58.9	926	12	BG755166
5	831.2	58.1	901	13	EM007892
6	830.4	58.0	988	14	BQ708857

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	824.4	57.6	1029	14	BQ063185	BQ063185	AGENCOURT
8	822.8	57.5	887	14	BQ711255	BQ711255	AGENCOURT
9	822.2	57.5	918	14	BQ708022	BQ708022	AGENCOURT
10	815.2	57.0	995	14	BM914540	BM914540	AGENCOURT
11	808.8	56.5	881	14	BQ711291	BQ711291	AGENCOURT
12	800.2	55.9	1031	14	BQ064886	BQ064886	AGENCOURT
13	800.2	55.7	936	14	BQ711727	BQ711727	AGENCOURT
14	796	55.6	940	14	BQ705928	BQ705928	AGENCOURT
15	787.4	55.0	977	14	BQ710532	BQ710532	AGENCOURT
16	786.4	55.0	980	14	BM914504	BM914504	AGENCOURT
17	785.2	54.9	843	13	BM007897	BM007897	603617582
18	778.8	54.4	991	14	BQ708936	BQ708936	AGENCOURT
19	777.2	54.3	973	14	BQ706204	BQ706204	AGENCOURT
20	772.6	54.0	930	13	BM007597	BM007597	603616995
21	770.6	53.9	981	14	BM914528	BM914528	AGENCOURT
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33	733.6	51.3	919	14	BQ709339	BQ709339	AGENCOURT
34	732.8	51.2	936	14	BQ707530	BQ707530	AGENCOURT
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ALIGNMENTS

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VERSION BQ062878.1 GI:19890085
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1020)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM2094 row: h column: 21
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Location/Qualifiers

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/lab_host="DH10B (phage-resistant)"
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
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Best Local Similarity 98.0%; Pred. No. 1.1e-204;
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VERSION BQ709771.1 GI:21848670
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 947)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM2466 row: m column: 16
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Location/Qualifiers
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into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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 QY 800 CGTCACT 859
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 QY 860 AGGTCAATGCGTGGTGGAGCTGAGCAGCAAGACACCTGAGGTCAAGTTCAACTGCT 919
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 VERSION BQ706140.1
 KEYWORDS GI:21845039

SOURCE EST.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 958)

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strauberg, Ph.D.

COMMENT Email: cgabs-f@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LCM2464 row: a column: 01
 High quality sequence stop: 705.

Location/Qualifiers

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 /note="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

BASE COUNT 229 a 319 c 256 g 150 t 4 others

ORIGIN

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 Best Local Similarity 99.2%; Pred. No. 2.2e-192;
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 QY 1158 GCTGACCAAGACCAAGGTGTGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1217
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QY 1278 GCTGGACTCGAGCGGCTCTTCTTCTCTACAGCAAGCTCACCCTGGAGAGAGAGTG 1337
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DEFINITION mRNA sequence.
ACCESSION BG755166
VERSION BG755166.1 GI:14065819
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 926)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-femail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1695 row: o column: 21
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Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC library."
BASE COUNT 225 a 309 c 244 g 148 t
ORIGIN

Query Match 58.9%; Score 842.4; DB 12; Length 926;
Best Local Similarity 98.2%; Pred. No. 1.8e-190;
Matches 852; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 564 CTCAGCGCCCTGACAGCGGCTGCACACCTTCCCGGCTGCTCCTACGCTCTCAGGACT 623
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RESULT 5
LOCUS BM007892
DEFINITION mRNA sequence.
ACCESSION BM007892
VERSION BM007892.1 GI:16522233
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 901)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: j column: 20
High quality sequence stop: 834.

FEATURES
source
1. 901
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/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 209 a 315 c 234 g 143 t
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Query Match 58.1%; Score 831.2; DB 13; Length 901;
Best Local Similarity 97.7%; Pred. No. 8.3e-188;
Matches 864; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

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QY 528 GACTACTTCCCGAACCGGTGACCGTGTGCGAACTCAGCGCCCTGACAGCGGGT 587
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QY 588 GCACACCTTCCCGGTGCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGAC 647
Db 199 GCACACCTTCCCGGTGCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGAC 258
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Db 259 CGTGCCTTCCAGCAGTGGGACCCAGACCTACATCTGCAACGTGAATCAACAGCCAG 318
QY 708 CAACACCAAGTGGACAGAAAGAGAGAGCCAAATCTTGTAACAAACTCACACATGCC 767
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QY 828 CAAGACACCTCATGATCTCCGAGACCCCTGAGTCAATCGGTGGTGGAGTGGAG 887
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Db 499 CCACGACACCTGAGTCAAGTTCAGTGTGAGTGGAGCGGTGGAGTGCATATGC 558
QY 948 CAAGACAAAGCCGGGAGGAGCAGTACAAAGCAGCTACCGTGGTGGTGGTGGTCTCAC 1007
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QY 1247 CGGAGAACCACTTCAAGACCAAGCCCTCCCGTGTGAGTCTCCGAC 1290
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RESULT 6
BQ708857
LOCUS BQ708857
DEFINITION BQ708857
ACCESSION BQ708857
VERSION BQ708857.1 GI:21847756
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2464 row: c column: 02
High quality sequence stop: 716.

FEATURES
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 230 a 338 c 258 g 162 t
ORIGIN
Query Match 58.0%; Score 830.4; DB 14; Length 988;
Best Local Similarity 94.6%; Pred. No. 1.3e-187;
Matches 904; Conservative 0; Mismatches 46; Indels 6; Gaps 4;

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Db 125 GGGTGCCTGGTCAAGGACTACTTCCCGAAGCGGTGAGGTGCTGCTGAACTCAGGCG 184
QY 573 CTGTACAGCGGGGCGTGCACACCTTCCCGGTGCTCTACAGTCTCTCAGGACTCTACTCCCT 632
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QY 813 CTTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCT 872
Db 425 CTTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCT 484
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ACCESSION BQ063185
VERSION BQ063185.1 GI:19890681
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 1029)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Rubin Laboratory
 cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCW2095 row: g column: 10
 High quality sequence stop: 723.

FEATURES

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 /tissue_type="lymphoma, cell line"
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 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

BASE COUNT 237 a 350 c 276 g 165 t 1 others

ORIGIN

Query Match 57.6%; Score 824.4; DB 14; Length 1029;
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 Matches 861; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

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 QY 903 GGTCAAGTTCAACTGTTACGTGGAGCGGTGGAGGTGATATGCAAGACAAAGCCGCG 962
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2469 row: i column: 20
High quality sequence stop: 667.
FEATURES
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."
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Best Local Similarity 95.4%; Pred. No. 1.2e-185;
Matches 867; Conservative 0; Mismatches 40; Indels 2; Gaps 2;
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DB 61 CGGTCTTCCCTCGCACCTCTCTCAAGAGCACTCTGGGGGACAGCGGCGCTGGGCT 120
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
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NIH-MGC <http://mgc.nci.nih.gov/>;
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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laboratory of Gerald M. Rubin (University of California,
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 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
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 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 977)
NIH-MGC <http://mgc.mci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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Location/Qualifiers

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 13:14:13 ; Search time 319.784 Seconds
(without alignments)
10077.457 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	18 AAT62510	Primatized anti-hu
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3	1431	100.0	1431	24 AAS17243	DNA sequence of a
4	1315.8	91.9	1431	18 AAT62513	Primatized anti-hu
5	1315.8	91.9	1431	19 AAV35489	Macaque primatized
6	1315.8	91.9	1431	24 AAS17247	DNA sequence of a
7	1246.4	87.1	1634	21 AAZ50012	Human immune syste
8	1237.2	86.5	1431	17 AAT18059	Monoclonal antibod
9	1234.8	86.3	1567	22 AAC66522	Human immune syste

10	1221.6	85.4	1418	17 AAT26889	Anti-rhesus D reco
11	1171.4	81.9	1404	18 AAT62868	Human gamma-4 heav
12	1168.2	81.6	1404	18 AAT62870	Human gamma-4PE he
13	1166.6	81.5	1404	18 AAT62869	Human gamma-4G hea
14	1135	79.3	1428	22 AAT74680	Nucleotide sequenc
15	1125.2	78.6	1428	18 AAT61241	Human anti-RSV mon
16	1124.2	78.6	1507	21 AAO3695	Human immunoglobul
17	1122.8	78.5	1430	24 AAK98701	cDNA of the heavy
18	1117.2	78.1	1437	19 AAV35487	Macaque primatized
19	1117.2	78.1	1437	24 AAS17245	DNA sequence of a
20	1115.6	78.0	1437	18 AAT13847	Primatized anti-hu
21	1115.4	77.9	1442	22 AAC84208	Plasmid Glambda-1B
22	1113.4	77.8	1798	21 AAC98220	Human colon cancer
23	1113.2	77.8	1644	22 AAS22593	Human CDNA encodin
24	1112.8	77.8	19035	19 AAV61794	Traget plasmid Man
25	1112.2	77.7	6281	22 AAC84206	Plasmid Glambda-1A
26	1110.8	77.6	1428	18 AAT61279	Human anti-RSV mon
27	1103.6	77.1	1617	14 AAQ35099	Antibody D heavy c
28	1103	77.1	1467	13 AAQ23570	Reshaped CAMPATH-1
29	1102	77.0	1599	24 ABK64550	Human benign prost
30	1102	77.0	1599	24 ABL62673	Colon adenocarcino
31	1102	77.0	1599	24 ABL65479	Lung cancer relate
32	1102	77.0	1599	24 ABL66294	Lung cancer relate
33	1100.8	76.9	1427	19 AAV41429	Plasmid Hu19Hcpod
34	1100.8	76.9	1427	19 AAV41431	Plasmid Hu19CHcpod
35	1098.8	76.8	1449	20 AAX08951	Monoclonal antibod
36	1098.8	76.8	1449	20 AAX06952	Monoclonal antibod
37	1097.6	76.7	1427	19 AAV41432	Plasmid Hu19Hcpod
38	1096.6	76.6	1612	22 AAS22482	Human CDNA encodin
39	1096	76.6	7521	22 AAF30315	Bicistronic chimer
40	1094	76.5	1549	13 AAQ20066	Encodes heavy chai
41	1093.8	76.4	1458	13 AAQ23571	Reshaped CD4 antib
42	1093.8	76.4	1458	13 AAQ23581	Reshaped CD4 antib
43	1092.8	76.4	6284	19 AAV41427	Plasmid Hu19AFcpod
44	1092.6	76.4	6557	17 AAT15932	Anti-IgE VH expres
45	1092.2	76.3	1617	24 AAS62784	cDNA sequence #571

ALIGNMENTS

RESULT 1
AAT62510
ID AAT62510 standard; DNA; 1431 BP.
XX
AC AAT62510;
XX
XX 25-MAY-1997 (first entry)
XX
DE Primatized anti-human B7.1 antigen antibody 7C10 heavy chain DNA.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW KW: primatized antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma; ss.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
PN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
PR 07-JUN-1995; 95US-0487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
XX Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX

Db	1081	ATCGAGAAAACCATCTCTCAAAGCCAAAGGGCAGCCCCCGAGAACCAACAGGTGTGTACACCTG	1140
Qy	1141	CCCCCATCCGGGATGAGCTGACCAAGAACCAAGCTCAGCTGCCTCGCTGGTCAAGGC	1200
Db	1141	CCCCCATCCGGGATGAGCTGACCAAGAACCAAGCTCAGCTGCCTCGTGTCAAGGC	1200
Qy	1201	TTCTATCCCAAGCAGCATCGCGTGGAGTGGGAGAGCAATCGGCGACGGGAGAACAACTAC	1260
Db	1201	TTCTATCCCAAGCGHATCTCGCTGGATGGGAGAGCAATGGGACGCCGAGAACAACTAC	1260
Qy	1261	AAGACCAAGCTCCCGTGTGGACTCCGACGGGTCTTCTTCTCTCTACCAAGCTCAAC	1320
Db	1261	AAGACCAAGCTCCCGTGTGGACTCCGACGGGTCTTCTTCTCTCTACCAAGCTCAAC	1320
Qy	1321	GTGGACAAGAGCAGGTGCGACGAGGGGAAGTCTTCTCATGCTCCGGTATGCATGAGGCT	1380
Db	1321	GTGGACAAGAGCAGGTGCGACGAGGGGAAGTCTTCTCATGCTCCGGTATGCATGAGGCT	1380
Qy	1381	CTGCACAACCACTACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAAATGA	1431
Db	1381	CTGCACAACCACTACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAAATGA	1431

RESULT 4

AA062513	
ID	AA062513 standard; DNA; 1431 BP.
XX	
XX	AA062513;
XX	
DT	25-MAY-1997 (first entry)
XX	
DE	Primitised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
XX	
KW	Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW	primitised antibody; B7 antigen; CD28; immunosuppressive;
KW	autoimmune disease; idiopathic thrombocytopenia purpura;
KW	systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW	type 1 diabetes mellitus; graft versus host disease;
KW	hetero-hybridoma; transfectoma; ss.
XX	
OS	Chimeric Macaca cynomolgus;
OS	Chimeric Homo sapiens.
XX	
PN	WO9640878-A1.
XX	
PD	19-DEC-1996.
XX	
PF	06-JUN-1996; 96WO-US10053.
XX	
PR	07-JUN-1995; 95US-0487550.
XX	
PA	(IDEC-) IDEC PHARM CORP.
XX	
PI	Anderson DR, Brams P, Hanna N, Shetowsky WS;
XX	
DR	WPI; 1997-108638/10.
DR	P-PSDB; AA01822.
XX	
PT	Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT	useful for treating autoimmune disease or graft-versus-host diseases
XX	
PS	Claim 11; Fig 10B; 81pp; English.
XX	
CC	2 DNA sequences (AA062512 and AA062513) respectively code for
CC	primitised forms (AA01821 and AA01822) of the light and heavy chain
CC	of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC	16C10. Cloned 16C10 light and heavy variable genes are inserted
CC	into an expression vector (pref. NEOSPUA) which contains human lig
CC	and heavy chain constant region genes to allow prodn. of primatised
CC	antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
CC	antibodies have also been produced (see also AA01817-20). The
CC	primitised antibodies inhibit the B7:CD28 pathway, making them
CC	useful immunosuppressants for the treatment of autoimmune disorder
CC	

[illegible]

Qy	1381	CTGCACAAACACTACACGACGAGAGCCTCTCCCTGTCTCCGGGTAATGA	1431
Db	1381	CTGCACAAACACTACACGACGAGAGCCTCTCCCTGTCTCCGGGTAATGA	1431
RESULT 7			
AAZ50012			
ID	AAZ50012	standard; cDNA; 1634 BP.	
XX	AC		
XX	AAZ50012;		
XX			
DT	25-APR-2000	(first entry)	
XX			
DE	Human immune system molecule, ISMO-2 cDNA.		
XX			
KW	Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;		
KW	treatment; prevention; cell proliferation; immune system disorder; ss		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	78..1490	
FT		/*tag= a	
FT		/product= "ISMO-2"	
FT		/note= "ISMO-2 shows homology to vertebrate	
FT		immunoglobulin gamma heavy-chain"	
FT	sig_peptide	78..134	
FT		/*tag= b	
FT	mat_peptide	135..1487	
FT		/*tag= c	
FT		/product= "Mature ISMO-2 protein"	
FT	misc_binding	432..473	
FT		/*tag= d	
FT		/bound_moiety= "Hybridisation probe"	
XX			
PN	W0200000608-A2.		
XX			
PD	06-JAN-2000.		
XX			
XX	21-JUN-1999;	99WO-US13995.	
XX			
PR	30-JUN-1998;	98US-0107223.	
XX			
PA	(INCY-) INCYTE PHARM INC.		
XX			
PI	Lal P, Tang YT, Corley NC, Gorgone G, Guegler KJ, Patterson C;		
PI	Baughn MR;		
XX			
DR	WPI; 2000-170916/15.		
DR	P-FSDB; AAY44721.		
XX			
PT	Immune system molecules used in the diagnosis, treatment and prevention		
PT	of disorders associated with the immune system and cell proliferation		
XX			
PS	Claim 7; Pages 64-65; 69pp; English.		
XX			
CC	The present sequence is a cDNA encoding an immune system molecule,		
CC	ISMO-2 from an Incyte clone 2849752 isolated from the human breast		
CC	tumour cDNA library (BRSTTUN13). This sequence is expressed in several		
CC	libraries, generally those associated with cancer, cell		
CC	proliferation, immune response or trauma.		
CC	The present sequence is useful in the diagnosis, treatment and		
CC	prevention of disorders associated with the immune system and		
CC	cell proliferation.		
CC			

Qy	1321	GTGGACAAGAGCAGGTGGCAGCAGGGAA	CGTCTTCTCATGCTCCGTCGATGCATGAGGCT	1380
Db	1294	GTGGACAAGAGCAGGTGGCAGCAGGGAA	TGCTTTCTCATGCTCCGTCGATGCATGAGGCT	1353
Qy	1381	CTGCACAACCACTACACGAGAAGAGGCT	CTCCCTGTCTCCGGTAAATGA	1431
Db	1354	CTGCACAACCACTACACAGAAGAGGCT	CTCCCTGTCTCTGGGTAAATGA	1404

RESULT 14	
AAH74680	
ID	AAH74680 standard; DNA; 1428 BP.
XX	
XX	
AC	AAH74680;
AC	
XX	
DT	29-OCT-2001 (first entry)
DT	
XX	
XX	Nucleotide sequence of a single chain antibody.
DE	
XX	
XX	Complementarity determining region; CDR; single chain antibody; ScFv;
KW	hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
KW	envelope glycoprotein; HCV.
KW	

OS	Homo sapiens.	
XX		
XX		
PH	Key	Location/Qualifiers
FT	CDS	1..1428
FT		/*tag= a
FT		/product= "single chain antibody"

PN WO200158459-A1.
XX
XX
PD 16-AUG-2001.
XX
XX 13-FEB-2001; 2001WO-JF00967.
XX
XX 14-FEB-2000; 2000JF-0034906.
XX
XX (MITS-) MITSUBISHI-TOKYO PHARM INC.
PA

XX	Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;
PI	
XX	WPI; 2001-496986/54.
XX	P-PSDB; AAG63640.
PT	Remedies for hepatitis C containing substances with antiviral effects
PT	e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
PT	compounds, by inhibiting binding of hepatitis C virus envelope
PT	glycoprotein, or CD81 -

Claim 41; Page 105-108; 138pp; Japanese.

The present sequence encodes a single chain antibody of the invention. The specification describes a substance can inhibit the binding between hepatitis C virus (HCV) and cells with potential HCV infection, cells with expression of CD81, or CD81. This substance is especially an antibody with affinity towards HCV E2/NS1 protein, containing amino acid sequences based on the complementarity determining region (CDR) CD82 and CD83 of the H and L chain variable regions. The antibody inhibits the viral envelope glycoprotein. It is also a CD81 inhibitor. The antibodies and drugs are used for treatment and/or prevention of hepatitis C, or for diagnosis of hepatitis C.

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	Matches 1253;	Conservative	0;	Mismatches	175;	Indels	3; Gaps 1;
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Db	1.	ATGAAACACCTGTGGTTCTTCTCTGTGTGTGCAGCTCCACATGGGTCCTGTCCAG	60				

QY	61	GTGAAGCTGAGCAGTGGGGGAGGAGCACTTCTGCAGCCTTTCGAGAGACCTGTGCCGACCC	120
Db	61	GTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCTTCGTTGAAGTCTCC	120
QY	121	TGCGTTGTCTCTGGTGGCTCCATCAGCGGTACTACTCTGGAACCTGGATCCGCCAGAGCC	180
Db	121	TGCAAGGCTTCTGGAGGACCTACATCG---ACCAACCTATCGGCTGGGTGCGACAGGCC	177
QY	181	CCAGGAGGGGACTGGAGTGGATTTGGCCATATTTATGGTTAAATGGTGCAGACCAACAATAC	240
Db	178	CCTGGACAAGGGCTTGGTGGATGGAGGGATCATCCCTCTCTCTGGTCCGCCACACTAC	237
QY	241	AATCCCTCCCTCAAGAGTCGAGTCCACATTTCAAAGACACGTCCTCAAGAACACAGTCTTTC	300
Db	238	GCACAGAAGTTCAGGGCAAAAGTCTCGATTCACGCGACGAGTTCACAGAGCAGCTTAC	297
QY	301	CTGAACCTTGAATTTCTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGAGAGCCCT	360
Db	298	CTGGAACCTGACAGCCCTCACATCTGAGGACACGGCCGTATATTACTGTGCGAGGTCTT	357
QY	361	CGCCCTGATTGCACAACCAATTTGTTATGGGGGTGGGTGATGTCTGGGGCCCGGAGAC	420
Db	358	AGGGGTATTGTGCTGCTGGTTCTGCTGATGACTGACTCGACCCCTCGGGGCCAAGGACCC	417
QY	421	CTGTGCACCGTCTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTTGGCACCTCC	480
Db	418	CTGTGCACCGTCTCAGTGTCTAGTACCAAGGGCCCATCCGTCTTCCCTTGGCACCTCC	477
QY	481	TCCAGAGCACTCTGGGGGCAACGCGCCCTGGGTGCTGGTCAAGACTACTTCCCTCC	540
Db	478	TCCAGAGCACTCTGGGGGCAACGCGCCCTGGGTGCTGGTCAAGACTACTTCCCTCC	537
QY	541	GAACCGGTGACCGTGTCTGGAACTCAGGGGCCCTGACCAAGCGGCTGCACACTTCCCG	600
Db	538	GAACCGGTGACCGTGTCTGGAACTCAGGGGCCCTGACCAAGCGGCTGCACACTTCCCG	597
QY	601	GCTGTCTCAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGCCTCCAGC	660
Db	598	GCTGTCTCAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGCCTCCAGC	657
QY	661	AGCTTGGGACCCAGACTACATCTGCAAGTGAATCAAGCCCGACGACCAACAGAGTG	720
Db	658	AGCTTGGGACCCAGACTACATCTGCAAGTGAATCAAGCCCGACGACCAACAGAGTG	717
QY	721	GACAAGAAAGCAGAGCCCAAAATCTGTGACAAATCTCACATGCCCAACCGTCCCGACGA	780
Db	718	GACAAGAAAGTGGAGCCCAAAATCTGTGACAAATCTCACATGCCCAACCGTCCCGACGA	777
QY	781	CTTGAACTCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCGCCCAAAACCCCAAGGACACCTC	840
Db	778	CTTGAACTCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCGCCCAAAACCCCAAGGACACCTC	837
QY	841	ATGATCTCCCGACCCCTCAGGTGCATCGGTGGTGGAGCTGAGCCACGAGAGACCT	900
Db	838	ATGATCTCCCGACCCCTCAGGTGCATCGGTGGTGGAGCTGAGCCACGAGAGACCT	897
QY	901	GAGGTCAAGTTCAACTGGTACCTGGACGCGGTGGAGGTGCAATAATGCCAAGACAAAGCCG	960
Db	898	GAGGTCAAGTTCAACTGGTACCTGGACGCGGTGGAGGTGCAATAATGCCAAGACAAAGCCG	957
QY	961	CGGGAGGAGGATPACAACAGCAGTACCGTGTGGTCAAGTCTCTCAACCGTCTGCAACCAG	1020
Db	958	CGGGAGGAGGATPACAACAGCAGTACCGGTGGTCAAGTCTCTCAACCGTCTGCAACCAG	1017
QY	1021	GACTGTCTGAATGGCAAGGATCAAGTGTCAAGGTCTCCAAACAAAGCCCTCCAGGCCCTC	1080
Db	1018	GACTGTCTGAATGGCAAGGATCAAGTGTCAAGGTCTCCAAACAAAGCCCTCCAGGCCCTC	1077
QY	1081	ATCGAGAAACCAATCTCCAAAGCCAAAGGGACCCCGAGAACCAAGTGTGACACCTGT	1140
Db	1078	ATCGAGAAACCAATCTCCAAAGCCAAAGGGACCCCGAGAACCAAGTGTGACACCTGT	1137

Qy	974	ACAACGACGTAACCGTGTGGTCAAGCGTCTCAACCGTCTTGACAACGAGACTGGCTGAATG	1033
Db	971	ACAACGACGTAACCGTGTGGTCAAGCGTCTCAACCGTCTTGACAACGAGACTGGCTGAATG	1030
Qy	1034	GCAAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCACAGCCCCCATCGAGAAACCA	1093
Db	1031	GCAAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCACAGCCCCCATCGAGAAACCA	1090
Qy	1094	TCTTCCAAGCCAAAGGCGACCCCGAGAACCAACAGGTGTACACCTTGC0CCCCATCCGGG	1153
Db	1091	TCTTCCAAGCCAAAGGCGACCCCGAGAACCAACAGGTGTACACCTTGC0CCCCATCCGGG	1150
Qy	1154	ATGAGCTGACCAAGAACACAGGTGAGCTGACCTGCTGTCAAGGCTTCTATCCACGG	1213
Db	1151	ATGAGCTGACCAAGAACACAGGTGAGCTGACCTGCTGTCAAGGCTTCTATCCACGG	1210
Qy	1214	ACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCCGGAGAACAACTACAAGACCAACGCCTC	1273
Db	1211	ACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCCGGAGAACAACTACAAGACCAACGCCTC	1270
Qy	1274	CCGTGCTGGAATCGGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA	1333
Db	1271	CCGTGCTGGAATCGGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA	1330
Qy	1334	GGTGGCAGCAGGGGAACGCTTCTCATGTCTCCGTGATGCATGAGGCTCTGTGCAACCACT	1393
Db	1331	GGTGGCAGCAGGGGAACGCTTCTCATGTCTCCGTGATGCATGAGGCTCTGTGCAACCACT	1390
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Db	1391	ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1428

Search completed: June 3, 2003, 14:45:36
Job time : 325.784 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 17:51:01 ; Search time 188.659 Seconds

(without alignments)
10227.493 Million cell updates/sec

Title: US-09-576-424-3

Perfect score: 1431

Sequence: 1 atgaacacctgtgtgtttt.....ccctgtctccgggtaaatga 1431

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	9	US-10-124-905-3
2	1431	100.0	1431	9	US-09-948-429B-3
3	1429.4	99.9	1431	9	US-10-073-138-2
4	1315.8	91.9	1431	9	US-10-124-905-11
5	1315.8	91.9	1431	9	US-09-948-429B-11
6	1314.2	91.8	1431	9	US-10-073-138-6
7	1171.4	81.9	1404	9	US-10-211-357-7
8	1168.2	81.6	1404	9	US-10-211-357-11
9	1166.6	81.5	1404	9	US-10-211-357-9
10	1123.6	78.5	1428	10	US-09-740-002-17
11	1117.2	78.1	1437	9	US-10-124-905-7
12	1117.2	78.1	1437	9	US-09-948-429B-7
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19	1100.8	76.9	1427	12	US-10-066-895-20

20	1100.8	76.9	1427	12	US-10-066-895-25	Sequence 25, Appl
21	1098.8	76.8	1449	10	US-09-747-669-1	Sequence 1, Appl
22	1098.8	76.8	1449	10	US-09-747-669-2	Sequence 2, Appl
23	1097.6	76.7	1427	12	US-10-066-895-27	Sequence 27, Appl
24	1092.8	76.4	6284	12	US-10-066-895-14	Sequence 14, Appl
25	1092.2	76.3	1617	10	US-09-822-830A-571	Sequence 571, App
26	1090.6	76.2	8120	9	US-09-726-258-68	Sequence 68, Appl
27	1089.2	76.1	1356	10	US-09-822-898A-27	Sequence 27, Appl
28	1088.8	76.1	1539	10	US-09-822-849A-87	Sequence 87, Appl
29	1087.6	76.0	1615	10	US-09-822-849A-111	Sequence 111, App
30	1087	76.0	9199	9	US-09-911-692-3	Sequence 3, Appl
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33	1087	76.0	9209	9	US-10-096-984-2	Sequence 2, Appl
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38	1083.8	75.7	9182	9	US-09-927-121B-89	Sequence 89, Appl
39	1081	75.5	1404	10	US-09-825-012-10	Sequence 10, Appl
40	1081	75.5	3300	9	US-10-020-786-2	Sequence 2, Appl
41	1078.4	75.4	2196	10	US-09-825-012-44	Sequence 44, Appl
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43	1078.4	75.4	2226	10	US-09-825-012-53	Sequence 53, Appl
44	1078.4	75.4	2226	10	US-09-825-012-54	Sequence 54, Appl
45	1078	75.3	1347	10	US-09-736-371B-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-10-124-905-3
; Sequence 3, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10124,905
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs

:	NAME:	Teskin, Robin L.		
:	REGISTRATION NUMBER:	35,030		
:	REFERENCE/DOCKET NUMBER:	012712-131		
:	TELECOMMUNICATION INFORMATION:			
:	TELEPHONE:	703-836-6620		
:	TELEFAX:	703-836-2021		
:	INFORMATION FOR SEQ ID NO:	3:		
:	SEQUENCE CHARACTERISTICS:			
:	LENGTH:	1431 base pairs		
:	TYPE:	nucleic acid		
:	STRAINEDNESS:	not relevant		
:	TOPOLOGY:	linear		
:	MOLECULE TYPE:	peptide		
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Best Local Similarity 100.0%; Pred. No. 0;				
Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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RESULT 14

US-09-299-230
; Sequence 230, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 230
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
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; LOCATION: (1798)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-230

Query Match 77.8%; Score 1113.4; DB 9; Length 1798;
Best Local Similarity 87.6%; Pred. No. 5.5e-298;
Matches 1232; Conservative 8; Mismatches 155; Indels 11; Gaps 2;
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Search completed: June 3, 2003, 23:03:39
Job time : 194.659 secs

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2	1315.8	91.9	1431	3	US-08-487-550-11	Sequence 11, Appl
3	1234.8	86.3	1567	3	US-09-049-672A-17	Sequence 17, Appl
4	1210.4	84.6	1418	4	US-08-793-450-7	Sequence 7, Appli
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6	1168.2	81.6	1404	3	US-08-523-894-11	Sequence 11, Appl
7	1166.6	81.5	1404	3	US-08-523-894-9	Sequence 9, Appli
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9	1123.6	78.5	1428	2	US-08-634-223-17	Sequence 17, Appl
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26	1103.6	77.1	1617	2	US-08-378-939-9	Sequence 9, Appli
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LOCATION: 1..1431
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Query Match 91.9%; Score 1315.8; DB 3; Length 1431;
Best Local Similarity 95.0%; Pred. No. 3.3e-312;
Matches 1359; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

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QY 1081 ATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGACACACAGGTGTACACCTG 1140
DB 1081 ATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGACACACAGGTGTACACCTG 1140
QY 1141 CCCCATCCCGGATGAGTGCACCAAGAAACAGAGTGCAGCTGCCTGTGTCAAAGC 1200
DB 1141 CCCCATCCCGGATGAGTGCACCAAGAAACAGAGTGCAGCTGCCTGTGTCAAAGC 1200
QY 1201 TTCTATCCAGCGCATCGCGTGGAGTGGGAGAGCAATGGGAGACCCCGAGAACTAC 1260
DB 1201 TTCTATCCAGCGCATCGCGTGGAGTGGGAGAGCAATGGGAGACCCCGAGAACTAC 1260
QY 1261 AAGACCGCTCCCGTGGTGGAGTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
DB 1261 AAGACCGCTCCCGTGGTGGAGTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
QY 1321 GTGGACAAAGAGCAGGTGGCAGCAGGGGAAACGCTTCTCATGCTCGTGCATGAGGCT 1380
DB 1321 GTGGACAAAGAGCAGGTGGCAGCAGGGGAAACGCTTCTCATGCTCGTGCATGAGGCT 1380
QY 1381 CTGCACAACTACTACACGACAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1431
DB 1381 CTGCACAACTACTACACGACAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1431
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RESULT 3

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US-09-049-672A-17
; Sequence 17, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Gueghier, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
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:	REGISTRATION NUMBER:	24,618
:	REFERENCE/DOCKET NUMBER:	660-118-0 PCT
:	TELECOMMUNICATION INFORMATION:	
:	TELEPHONE:	703-413-3000
:	TELEFAX:	703-413-2220
:	INFORMATION FOR SEQ ID NO:	7:
:	SEQUENCE CHARACTERISTICS:	
:	LENGTH:	1418 base pairs
:	TYPE:	nucleic acid
:	STRANDEDNESS:	single
:	TOPOLOGY:	linear
:	MOLECULE TYPE:	other nucleic acid
:	FEATURE:	
:	NAME/KEY:	CDS
:	LOCATION:	1..1418
:	FEATURE:	
:	NAME/KEY:	sig_peptide
:	LOCATION:	1..57
:	FEATURE:	
:	NAME/KEY:	mat_peptide
:	LOCATION:	58..1418
:	OTHER INFORMATION:	/product= "IMMUNOGLOBIN, HEAVY"
:	OTHER INFORMATION:	CHAIN"
:	US-08-793-450-7	

Query Match	84.6%;	Score 1210.4;	DB 4;	Length 1418;
Best Local Similarity	92.4%;	Pred. No. 1.8e-286;		
Matches 1310;	Conservative 0;	Mismatches 96;	Indels 12;	Gaps 3

Qy	13	TGGTTCCTCCCTCCTCGGTGGCGAGCTCCACAGATGGGTCCTGTGCCAGGTGAAGCTGCAG	72
Dd	13	TGTATCATCTCTCTCTTGTTGGTAGCACAGCTACAGGTGTCCAATCCCAAGTCCAATTGGAG	72
Qy	73	CAGTGGGGCGAAGAACTTCTGCAGCCTTTCGAGACCCTGTCCCCGACCTCGGTGTCTCTCT	132
Dd	73	CAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCCTCACTGCACCTGTCTAT	132
Qy	133	GGTGGCTCCATCAGCGGTTACTACTCTGACCTGGATCCGCCAGACCCACGGAGGGGA	192
Dd	133	GGTGGGTCCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCCCCAGGGGAAGGGG	189
Qy	193	CTGGAGTGGATTGGCCCATATTTATGGTAATGGTGGACCCACCACTACAATCCCTCCCTC	252
Dd	190	CTGGAGTGGATTGGGAATACAA---TCATAGTGAAGCAACCACTACAACCCGCTCCCTC	246
Qy	253	AAGAGTCGAGTCACATTTCAAAAAGACAGCTCCAAGAACCAGTTCTTCTGAACTTGAAT	312
Dd	247	AAGAGTCGAGTCACCATATCATAGTAGACACGTCGAAGAACCAGTTCTTCCCTGAAACTGAAC	306
Qy	313	TCTGTGACCGACGGGACACGGCCGTCTATTACTGTGCGAGAGGCCCTCGCCCTGATTGC	372
Dd	307	TCTGTGACCGCCGGACACGGCTGTGTATTACTGTGCGAGGG-----CCCCAGAGTAT	360
Qy	373	ACRACCATTTGTTATGGCGGCTGGGTTCGATGCTCTGGGCGCCGGGAGACCTGTGTACCCGTC	432
Dd	361	AAATGGAAGTATCATGGSAGCTGGTTCGACCCCTGGGSCCAAGGTATCACTGTACCGTC	420
Qy	433	TCCTCAGCTAGCACAAAGGGCCCATCGGTCTTTCGCCCTTGGCAACCTCTCTCCAAGAGCAAC	492
Dd	421	TCCTCAGCCTCCACCAAGGGGCCATCGGTCTTTCGCCCTTGGCAACCTCTCTCCAAGAGCAAC	480
Qy	493	TCTGGGGGCAACAGCGGCCCTGGGCTGTGCTGTCAAGGACTACTTCCCAGAACCGGTGACG	552
Dd	481	TCTGGGGGCAACAGCGGCCCTGGGCTGTGCTGTCAAGGACTACTTCCCAGAACCGGTGACG	540
Qy	553	GTGTCTGTGGAATCAGGCGCCCTGACACAGCGCGGTGCACACTTCCCAGGCTGTCTCTACAG	612
Dd	541	GTGTCTGTGGAATCAGGCGCCCTGACACAGCGCGGTGCACACTTCCCAGGCTGTCTCTACAG	600
Qy	613	TCCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTCTCAGCAGCTTGGGCAAC	672
Dd	601	TCCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTCTCAGCAGCTTGGGCAAC	660

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-838-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain variable and constant gamma
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1404
US-08-523-894-7

Query Match 81.9%; Score 1171.4; DB 3; Length 1404;
Best Local Similarity 90.0%; Pred. No. 5.9e-277;
Matches 1288; Conservative 0; Mismatches 116; Indels 27; Gaps 2;

QY 1 ATGAACACCTGTTCTCTCTCTGTTGGAGCTCCAGATGGTCTCTGCCAG 60
DB 1 ATGAACACCTGTTCTCTCTCTGTTGGAGCTCCAGATGGTCTCTGCCAG 60
QY 61 GTGAAGTTCACAGTGGGGGCAAGACTTCTGCAAGCTTCGGAGACCTGTCGGCACC 120
DB 61 GTGCAAGTTCAGAGTGGGGGCAAGACTTCTGCAAGCTTCGGAGACCTGTCGGCACC 120
QY 121 TGCAGTGTCTCTGTTGGTCCATCAGCGTTACTACTGAGACCTGGATCCGCCAGACC 180
DB 121 TGCAGTGTCTCTGTTGGTCCATCAGCGTTACTACTGAGACCTGGATCCGCCAGTCC 180
QY 181 CCAGGAGGGGACTGAGTGGATTTGGCCATATTTATGTAATGGTGGACACCAACTAC 240
DB 181 CCAGGAGGGGACTGAGTGGATTCGCTACATCTATGTCAGTGGTGGGGGCAACCAATTAC 240
QY 241 ATCCCTCCCTCAAGTTCAGTCCACCATTTCAAAGACAGCTCCCAAGACCAAGTCTTC 300
DB 241 ATCCCTCCCTCAAGTTCAGTTCCTCAATTAAGACAGCTCCCAAGACCAAGTCTTC 300
QY 301 CTGAATCTTGAATTTCTGTACCCGACGCGGCGCTTATTAATGTCGAGAGGCGCT 360
DB 301 CTGAATCTTGAATTTCTGTACCCGACGCGGCGCTTATTAATGTCGAGAGGCGCT 360
QY 361 CGCCCTGATGTCACCAACATTTGTTATGGCGGCTGGGTGATGTCGGGGCCCGGGAGAC 420
DB 361 CGCCCTGATGTCACCAACATTTGTTATGGCGGCTGGGTGATGTCGGGGCCCGGGAGAC 420
QY 421 CTGTCACCGTCTCTCAGTACAGACAGGCGCCATCGTCTTCCCTTCCCTGACCCCTCC 480
DB 421 CTGTCACCGTCTCTCAGTACAGACAGGCGCCATCGTCTTCCCTTCCCTGACCCCTCC 480
QY 481 TCCAGAGACCTCTCTGGGGGACAGCGGCGCTGCTGGTCAAGAGACTTACTTCCCC 540
DB 481 TCCAGAGACCTCTCTGGGGGACAGCGGCGCTGCTGGTCAAGAGACTTACTTCCCC 540
QY 541 GAACCGGTGACGGTGTCTGTGAATCTCAGCGGCGCTGACAGCGGCGGTGCACACCTTCCCG 600

DB 523 GAACCGGTGACGGTGTCTGTGAATCTCAGGGCCCTGACACGCGGCTGCACACCTTCCCG 582
QY 601 GCTGTCTTACAGTCTCTCAGGACTTCTACTCTCTCAGCAGCGTGGTACCGTCCCTCCAGC 660
DB 583 GCTGTCTTACAGTCTCTCAGGACTTCTACTCTCTCAGCAGCGTGGTACCGTCCCTCCAGC 642
QY 661 AGCTTGGGACCCAGACCTACATCTGCAACGTGAATCAAGCCCGAGCAACCAAGGTG 720
DB 643 AGCTTGGGACCAAGAGACCTACACCTGCAACGTGAATCAAGCCCGAGCAACCAAGGTG 702
QY 721 GACAAGAAAGCAGAGAGCCCAATCTTGTGCAAAACTCACATGCTCCACCGTGGCCAGCA 780
DB 703 GACAAGAGAGTGTGATCCAAATATATG-----TCCCCATGCCATCATGTCGCCAGCA 753
QY 781 CCTGAATCTCTGGGGGACCGTCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
DB 754 CTTGATTTCTTGGGGGACCAATCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 813
QY 841 ATGATCTCTCCGGACCCCTGAGGTCAATGCTGGTGGTGGAGCTGAGCCAGAAAGCCCT 900
DB 814 ATGATCTCTCCGGACCCCTGAGGTCAAGTCAAGTCAAGTCTCTCTCTCTCTCTCTCTCTCT 873
QY 901 GAGTCAAGTTCAACTGTGTAGTGGACGGCTGAGGTGAGTCAATGCTCCAAAGAGCCG 960
DB 874 GAGTCCAGTTTCAACTGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 933
QY 961 CGGAGGAGGAGTACAAACAGCAGCTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB 934 CGGAGGAGGAGTTCAAACAGCAGCTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 993
QY 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
DB 994 GACTGGCTGAACGCAAGGAGTACAAGTGAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1053
QY 1081 ATCAGAAAACCATCTCTCAAGCCAAAGGGCAGCCCGAGAGAACCAAGGTGTACACCTG 1140
DB 1054 ATCAGAAAACCATCTCTCAAGCCAAAGGGCAGCCCGAGAGAACCAAGGTGTACACCTG 1113
QY 1141 CCCCCTCCCGGATGAGTGAACCAAGAACAGGTGAGCTGAGCTGCTCTCTCTCTCTCTCTCTCT 1200
DB 1114 CCCCCTCCCGGAGGAGTGAACCAAGAACAGGTGAGCTGAGCTGCTCTCTCTCTCTCTCTCT 1173
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DB 1174 TTCTATCCCGACGACATCGCGTGGAGTGGAGAGCAATGGGAGCCGAGGAAACAACCTAC 1233
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QY 1321 GTGACAGAGCAGGTGGCAGCAGGGGAAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
DB 1294 GTGACAGAGCAGGTGGCAGGAGGGAATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1353
QY 1381 CTGCACCAACCACTACACGACAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1431
DB 1354 CTGCACCAACCACTACACAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1404

RESULT 6

US-08-523-894-11
; Sequence 11, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Refi, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

Db 1354 CTGCACACACCTACACACAGAGAGCCCTCTCCCTGTCTCTGGGTAAATGA 1404
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RESULT 8
US-08-488-376-17
; Sequence 17, Application US/08488376
; Patent No. 5811524
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1428
US-08-488-376-17
Query Match 78.5%; Score 1123.6; DB 1; Length 1428;
Best Local Similarity 88.5%; Pred. No. 2.8e-265;
Matches 1255; Conservative 0; Mismatches 154; Indels 9; Gaps 3;
QY 17 TCTTCTCTCTCTGTGGCAGCTCCAGATGGTCTGTCCAGGTGAAGCTGCAGCAGT 76
Db 17 TCTTGTCTTCTTGTGCGTGTGTACCGGTGTCTGTCCAGGTGCAGTTGCAGGAGT 76
QY 77 GGGGCGAAGGACTTCTGCAGCCTTCGGAGACCTGTCCCGACCTGTGCTGGGTG 136
Db 77 CTGGTCTGTGTGTGAACCCACAGAGACCTCAGCTGACCTGCACCGTCTCTGGT 136
QY 137 GCTC---CATAGCGGTACTACTTGGACCTGATCCGCGAGACCCAGGAGGGGAC 193
Db 137 TCTCACTCAGCAACCTAGAAATGGGTGTGACCTGGATCCGTCCAGCCCGGGGAAGGCC 196
QY 194 TGGAGTGGATGGCCATATTTATGTTATGTTGGCGACCACTACATCTCCCTCA 253
Db 197 TAGAATGGCTTGGAAACATTTTTTCGAGTGCAGAAAGTC---CTTCACTCTCTCTGA 253

QY 254 AGAGTCGAGTCAACCATTTTCAAAGACAGCTCCAGAAACAGTTCCTGAACTTGAAT 313
Db 254 AGAGCAGACTCACACCTCCAGGACACCTCCAGAAAGCAGGTGGTCTTAAGCTTGACCA 313
QY 314 CTGTGACCGACGCGACACGCGCTATTACTGTGCGAGAGGCGCTCGCCCTGATTGCA 373
Db 314 ACGTGGACCTGTGGACACAGCCACATATTACTGTGCG---ACGGGTAGGACTGTATGACA 370
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Db 431 CCTAGCTAGACACAAAGGCGCCATCGGTCTTCCCTCTGGCACCTCTCTCAAGAGACCT 490
QY 494 CTGGGGGACACAGCGCGCTGGGTCTGCTGCTCAAGAGCTACTTCCCGAACCCTGACCG 553
Db 491 CTGGGGGACACAGCGCGCTGGGTCTGCTGCTCAAGAGCTACTTCCCGAACCCTGACCG 550
QY 554 TGTCTGGAACCTCAGCGCGCTTGACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGT 613
Db 551 TGTCTGGAACCTCAGCGCGCTTGACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGT 610
QY 614 CCTCAGACTCTACTTCCCTCAGCAGCGGTGTGACCGTGCCTTCCAGCAGCTTTGGGACCC 673
Db 611 CCTCAGACTCTACTTCCCTCAGCAGCGGTGTGACCGTGCCTTCCAGCAGCTTTGGGACCC 670
QY 674 AGACCTATCTGCAACCTGATCAAGCCCCAGCAACACCAAGGTGGACAGAAAGCAG 733
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QY 734 AGCCCCAAATCTTGTGACAAAACCTCACATATGCCACCGTCCAGCAGCTTGAACCTCTGG 793
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QY 794 GGGGACCGTCACTTCTTCTTCCCAAAACCAAGGACACCTCATGATCTCCCGGA 853
Db 791 GGGGACCGTCACTTCTTCTTCCCAAAACCAAGGACACCTCATGATCTCCCGGA 850
QY 854 CCCCTGAGTCACTGCTGTGGTGGAGCTGAGCCAGAACACCTTGAAGTCAAGTTCA 913
Db 851 CCCCTGAGTCACTGCTGTGGTGGAGCTGAGCCAGAACACCTTGAAGTCAAGTTCA 910
QY 914 ACTGTACGTGGACGCGTGGAGGTGCATAATGCCAAGAACGCGGGAGGAGCAGT 973
Db 911 ACTGTACGTGGACGCGTGGAGGTGCATAATGCCAAGAACGCGGGAGGAGCAGT 970
QY 974 ACAACAGCAGTACCGTGTGGTTCAGCTCTTCAACCGTCTTCCAGCAGGACTGGTGAATG 1033
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QY 1214 ACATCGCGTGGAGTGGAGAGCAATGGGAGCCGAGAACAACTACAGACACAGCCTC 1273
Db 1211 ACATCGCGTGGAGTGGAGAGCAATGGGAGCCGAGAACAACTACAGACACAGCCTC 1270
QY 1274 CCGTCTGAGTCTCCGACCGCTCTTCTTCTTACAGAAAGCTACCGTGGACAGAGCA 1333
Db 1271 CCGTCTGAGTCTCCGACCGCTCTTCTTCTTACAGAAAGCTACCGTGGAGAGAGCA 1330

QY 1334 GGTGGCAGCAGGGAACGCTCTCTCATGTCCGTGATGATGAGGCTCTGCACCAACT 1393
DB 1331 GGTGGCAGCAGGGAACGCTCTCTCATGTCCGTGATGATGAGGCTCTGCACCAACT 1390
QY 1394 ACACGAGAGAGCCTCTCCCTGTCTCCGGTAAATGA 1431
DB 1391 ACACGAGAGAGCCTCTCCCTGTCTCCGGTAAATGA 1428

RESULT 9
US-08-634-223-17
; Sequence 17, Application US/08634223
; Patent No. 5840298
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,223
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,376
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1428
US-08-634-223-17

Query Match 78.5%; Score 1123.6; DB 2; Length 1428;
Best Local Similarity 88.5%; Pred. No. 2.8e-265;
Matches 1255; Conservative 0; Mismatches 154; Indels 9; Gaps 3;

QY 17 TCTTCTCTCTCTGTGGCAGCTCCAGATGGGTCTCTGTCCAGGTGAAGCTGCAGCAGT 76
DB 17 TCTTCTCTCTCTGTGGTGTGTGTACGGGTCTCTGTCCAGGTGCAGGTGGCAGGAGT 76
QY 77 GGGGCGAAGGACTTCTGAGCCTTCGGAGACCTGTCCCGCACCTCGGTGTCTCTGTG 136
DB 77 CTGGTCTGTGGTGTGAACCCACAGAGACCTTCACGCTGACCTGCACCTGCTCTGGGT 136

QY 137 GCTC---CATCAGCGTTTACTACTGACCTGGATCCGCAGACCCCGAGGAGGGGAC 193
DB 137 TCTCACTCAGCAACCTAGATGGGTGTGACTGTATCGGTGAGCCCGCCCGGGAAGGGCC 196
QY 194 TGGAGTGGATTGGCCATATTTATGTAATGTGTGCACCAACCACTACAAATCCCTCCCTCA 253
DB 197 TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAAGTC---CTTCAGTCTCTCTGA 253
QY 254 AGAGTCGAGTCACCATTTTCAAAAGACACGTCCAAGAACAGTCTTCTCTGAATTTGAATT 313
DB 254 AGAGCAGACTCACCACTCTCCAGGACACCTCCAGAAGCCAGGTGGTCTCAAGCTTGACCA 313
QY 314 CTGTGACCGCAGCGGACACACGCGCTATTACTGTGCGAGAGGCGCTCGCCCTGATGCA 373
DB 314 AGTGGACCTGTGTGACACACGACCATATTACTGTGC---ACGGGTAGAGCTGTATGACA 370
QY 374 CAACATTTGTATGGCGGCTGGGTGATGTCTGGGGCCCGGGAGACCTGTGTCACCGTCT 433
DB 371 TCAATGCTTATTACCTATACTACCTGGATTATTGGGGGCGAGGAACCTGTGTCACCGTCT 430
QY 434 CTTGAGCTAGCACCAAGGCGCCCATCGGTCTTCCCGCTGGCACCTCTCTCCAGAGACCT 493
DB 431 CTTGAGCTAGCACCAAGGCGCCCATCGGTCTTCCCGCTGGCACCTCTCTCCAGAGACCT 490
QY 494 CTGGGGGCACAGCGGCGCTGGGCTGCCCTGGTCAAGGACTTACTTCCCGAAACCGGTGACGG 553
DB 491 CTGGGGGCACAGCGGCGCTGGGCTGCCCTGGTCAAGGACTTACTTCCCGAAACCGGTGACGG 550
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DB 551 TGTCTGGAACTCAGGCGCGCTGACACGCGGCTGCACACCTTCCCGGCTGTCTTACAGT 610
QY 614 CTTGAGGACTCTCTCTCCTCAGCAGCTGTGTGACCGTGCCTCTCAGCAGCTTGGGACCC 673
DB 611 CTTGAGGACTCTCTCTCCTCAGCAGCTGTGTGACCGTGCCTCTCAGCAGCTTGGGACCC 670
QY 674 AGACCTACATCTGCAACCTGTAATCAGAGCCAGCAACCAAGGTGACAGGAAGCAG 733
DB 671 AGACCTACATCTGCAACCTGTAATCAGAGCCAGCAACCAAGGTGACAGGAAGCAG 730
QY 734 AGCCCAATCTTGTGACAAAACCTCACAATGCCCAACCGTGGCCAGACCTTGAATCTCTGG 793
DB 731 AGCCCAATCTTGTGACAAAACCTCACAATGCCCAACCGTGGCCAGACCTTGAATCTCTGG 790
QY 794 GGGGACCGTCACTCTCTCTCTTCCCGCCAAACCCAGGACACCTCATGATCTCCCGGA 853
DB 791 GGGGACCGTCACTCTCTCTTCCCGCCAAACCCAGGACACCTCATGATCTCCCGGA 850
QY 854 CCCCTGAGGTCAATCGTGTGTGTGGACGTGAGCCAGGAAGACCTCAGGTCAAGTTCA 913
DB 851 CCCCTGAGGTCAATCGTGTGTGTGGACGTGAGCCAGGAAGACCTCAGGTCAAGTTCA 910
QY 914 ACTGTGACGTGGACCGGCTGGAGGTGCAATAATGCCAAGACAAAGCCGGGAGGAGCAGT 973
DB 911 ACTGTGACGTGGACCGGCTGGAGGTGCAATAATGCCAAGACAAAGCCGGGAGGAGCAGT 970
QY 974 ACAACAGCACGTACCGT 1033
DB 971 ACAACAGCACGTACCGT 1030
QY 1034 GCAAGGAGTCAAGTGCAGAGGTCTCCACAAAGCCCTCCAGCCCGCCATCCGAGAAACCA 1093
DB 1031 GCAAGGAGTCAAGTGCAGAGGTCTCCACAAAGCCCTCCAGCCCGCCATCCGAGAAACCA 1090
QY 1094 TCTCCAAAGCAAAGGCGAGCCCGGAGAACACAGGTGTATACCTGTGCCCGCATCCCGGG 1153
DB 1091 TCTCCAAAGCAAAGGCGAGCCCGGAGAACACAGGTGTATACCTGTGCCCGCATCCCGGG 1150
QY 1154 ATGAGCTGACCAAGAACACAGGT 1213
DB 1151 ATGAGCTGACCAAGAACACAGGT 1210

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